



Docket No.: N0008.0001  
(PATENT)

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

Patent Application of: Tadatake Oku et al.

Application No.: 10/507,156

Group Art Unit: Not Yet Assigned

Filed: September 7, 2004

Examiner: Not Yet Assigned

For: NOVEL HEME PEPTIDE

**RESPONSE TO RAW SEQUENCE LISTING ERROR REPORT**

Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

Dear Sir:

In response to the "Raw Sequence Listing Error Report" ("Report") received December 30, 2005 and pursuant to 37 C.F.R. § 1.825(a) and (b) and 37 C.F.R. § 1.821(g), submitted herewith is a substitute sequence listing in paper form (substitute sheets) and computer readable form (CRF), in which the errors indicated by the Report have been corrected. The "Statement to Support Filing and Submission in Accordance with 37 C.F.R. §§ 1.821-1.825" is also attached hereto.

The Applicants were advised by Ms. Christine Washington

Dated: February 27, 2006

Respectfully submitted,

By   
Charles E. Miller

DICKSTEIN SHAPIRO MORIN &  
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(212) 835-1400  
Attorney for Applicant

Attachments: Sequence Listing substitute sheets (7 pages); and  
CRF



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Atty. Docket No: N0008.0001

In re patent application of

OKU, TADATAKE et al.

Serial No. 10/507,156

Filed: September 7, 2004

For: NOVEL HEME PEPTIDE

STATEMENT TO SUPPORT FILING AND SUBMISSION IN  
ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825

Commissioner for Patents  
P.O. Box 1450  
Alexandria, Virginia 22313-1450  
Mail Stop SEQUENCE

Sir:

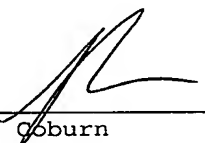
In connection with a Sequence Listing submitted concurrently herewith, the undersigned hereby states that:

1. the submission, filed herewith in accordance with 37 C.F.R. § 1.821(g), does not include new matter;

2. the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same.

Respectfully submitted,

Feb. 6, 2006  
Date

  
James A. Coburn

HARBOR CONSULTING IP SERVICES, INC.  
1500A Lafayette Road, #262  
Portsmouth, N.H. 03801  
800-318-3021



## STIC Biotechnology Systems Branch

### RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/507,156  
Source: PG 10  
Date Processed by STIC: 11/21/05

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebs/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

*Received 12/30/05.*

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

10/507,156

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."  
     Wrapped Aminos
- 2      Invalid Line Length    The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.  
     Numbering
- 4      Non-ASCII    The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length    Sequence(s)          contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0    A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)         . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.  
     "bug"
- 7      Skipped Sequences    Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence:  
     (OLD RULES)    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                     (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                     (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                     This sequence is intentionally skipped  
                     Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences    Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence.  
     (NEW RULES)    <210> sequence id number  
                     <400> sequence id number  
                     000
- 9      Use of n's or Xaa's    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     (NEW RULES)    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                     In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>    Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or  
     Response    scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>    Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses.  
     →    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
     (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0    Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.  
     "bug"
- 13      Misuse of n/Xaa    "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/507,156

DATE: 11/21/2005

TIME: 15:43:04

Input Set : A:\N0008001.app

Output Set : N:\CRF4\11212005\J507156.raw

3 <110> APPLICANT: OKU, TADATAKE  
 4 NISHIO, TOSHIYUKI  
 5 KAWACHI, RYU  
 6 SURUGA, KOHEI  
 8 <120> TITLE OF INVENTION: NOVEL HEME PEPTIDE  
 10 <130> FILE REFERENCE: N0008.0001  
 12 <140> CURRENT APPLICATION NUMBER: 10/507,156  
 13 <141> CURRENT FILING DATE: 2004-09-07  
 15 <150> PRIOR APPLICATION NUMBER: PCT/JP03/02394  
 16 <151> PRIOR FILING DATE: 2003-02-28  
 18 <150> PRIOR APPLICATION NUMBER: JP 2002-058086  
 19 <151> PRIOR FILING DATE: 2002-03-04  
 21 <160> NUMBER OF SEQ ID NOS: 18  
 23 <170> SOFTWARE: PatentIn Ver. 3.2

Does Not Comply  
Corrected Diskette Needed

## ERRORED SEQUENCES

335 <210> SEQ ID NO: 14  
 336 <211> LENGTH: 18 4 shown below  
 337 <212> TYPE: PRT  
 338 <213> ORGANISM: Artificial Sequence  
 340 <220> FEATURE:  
 341 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 342 peptide  
 344 <400> SEQUENCE: 14  
 E--> 345 Thr Val Glu Lys

(see p.2)

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2

<210> 11  
<211> 75  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Formula  
peptide

<220>

<221> MISC\_FEATURE

<222> (1)..(20)

<223> this region may encompass a hydrogen atom or 1-20 variable amino acids

<220>

<221> MISC\_FEATURE

<222> (22)..(23)

<223> any amino acid

<220>

<221> MISC\_FEATURE

<222> (25)

<223> His, Lys or Arg

<220>

<221> MISC\_FEATURE

<222> (26)..(75)

<223> this region may encompass a hydroxyl group or 1-50 variable amino acids

<220>

<223> see specification as filed for detailed description of preferred embodiments

<400> 11

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
1 5 10 15

Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
65 70 75

insufficient explanation  
(give source of genetic material-  
see item 11 on Error  
summary sheet)

this is OK

Xaa can only represent  
a single amino acid,  
nothing else. This  
error appears  
in subsequent  
sequences.

OK

This error  
appears  
in  
subsequent  
sequences

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/507,156

DATE: 11/21/2005

TIME: 15:43:05

Input Set : A:\N0008001.app

Output Set: N:\CRF4\11212005\J507156.raw

L:220 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0  
L:223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:16  
L:226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:32  
L:229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:48  
L:232 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:64  
L:272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0  
L:275 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:16  
L:278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:32  
L:281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:48  
L:284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:64  
L:319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0  
L:322 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:16  
L:325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:32  
L:328 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:48  
L:331 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:64  
L:345 M:252 E: No. of Seq. differs, <211> LENGTH:Input:18 Found:4 SEQ:14